

GAATTCCAGTGTGGCTTCACCTGCAGCACACTCCTGGCAAGGACCTGAGACCCCTGTGCTAACTC

1
AAGAGGCTCAATGGGCTGCAGAAGAACTAGAGAAGGACCAAGCAAGGCC
10
MET ILE PHE PRO TRP LYS [CYS] TGT
ILE PHE PRO TRP LYS [CYS] TGT
ATG ATA TTT CCA TGG AAA TGT

20
GLN SER THR GLN ARG ASP LEU TRP ASN ILE PHE LYS [CYS] TGT
CAG AGC ACC CAG AGG GAC TTA TGG AAC ATC TTC AAG
LEU TRP GLY TRP THR MET LEU [CYS] TGT
TTG TGG GGG TGG ACA ATG CTC

30
[CYS] ASP PHE LEU ALA HIS HIS GLY THR TYR [CYS] TGT
TGT GAT TTC CTG GCA CAT CAT GGA ACC TAC [TGC] TGG ACT TAC CAT TAT TCT GAA AAA CCC
PROBABLE N-TERMINUS

40
MET ASN TRP GLN ARG ALA ARG ARG PHE [CYS] TGC ARG ASP ASN TYR THR ASP LEU VAL ALA ILE
ATG AAC TGG CAA AGG GCT AGA AGA TTC [TGC] CGA GAC AAT TAC ACA GAT TTA GTT GCC ATA

50
GLN ASN LYS ALA GLU ILE GLU TYR LEU GLU LYS THR LEU PRO PHE SER ARG SER TYR TYR
CAA AAC AAG GCG GAA ATT GAG TAT CTG GAG AAG ACT CTG CCC TTC AGT CGT TCT TAC TAA

60
70
TRP ILE GLY ILE ARG LYS ILE GLY GLY ILE TRP THR TRP VAL GLY THR ASN LYS SER LEU
TGG ATA GGA ATC CGG AAG ATA GGA GGA ATA TGG AGC TGG GTG GGA ACC AAC AAA TCT CTC

80
90
THR GLU GLU ALA GLU ASN TRP GLY ASP GLY GLU PRO ASN ASN LYS LYS ASN LYS GLU ASP
ACT GAA GAA GCA GAG AAC TGG GGA GAT GGT GAG CCC AAC AAC AAG AAC AAG AAC GAG GAC
100

110
120
130
140
150

160
HIS LYS LEU LYS ALA ALA LEU [CYS] TYR THR ALA SER [CYS] GLN PRO TRP SER [CYS] SER GLN
CAC A-A C-T A-A G-A G-C-G-C-T-C-T-G-T-A-C-A G-C-T-C-T-G-C-A-G-C-T-C-A-G-T-C-A-G-T-C-G-C

FIG. 1A

170	HIS GLY GLU	CYS	VAL GLU ILE ILE ASN	ASN HIS THR	CYS	ASN CYS	ASP VAL GLY TYR	TYR
	CAT GGA GAA	TGT	GTA GAA ATC ATC AAT	AAT CAC ACC	TGC	TGT	GAT GTG GGG	TAC TAT
190	GLY PRO GLN	CYS	GLN LEU VAL ILE GLN	CYS	GLU PRO LEU GLU ALA	PRO GLU LEU GLY	THR	THR
	GGG CCC CAG	TGT	CAG CTT GTG ATT CAG	TGT	GAG CCT TTG GAG	GCC CCA GAG	CTG GGT	ACC
210	MET ASP	CYS	THR HIS PRO PHE GLY	ASN PHE SER	PHE SER SER	GLN CYS	ALA PHE SER	CYS
	ATG GAC	TGT	ACT CAC CCC TTT GGA	AAC TTC AGC	TTC AGC	TCA CAG	TGT	AAC TGG
230	SER GLU GLY	THR ASN LEU THR	GLY ILE GLU GLU	THR THR	CYS GLY	PRO PHE GLY	ASN TRP	
	TCT GAA GGA	ACA AAC TTA ACT	GGG ATT GAA GAA	ACC ACC	TGT GGA	CCA TTT GGA	AAC TGG	
250	SER SER PRO GLU PRO THR	CYS	GLN VAL ILE GLN	CYS	GLU PRO LEU SER	ALA PRO ASP LEU		
	TCA TCT CCA GAA CCA ACC	TGT	CAA GTG ATT CAG	TGT	GAG CCT CTA TCA GCA	CCA GAT TTG		
270	GLY ILE MET ASN	CYS SER	HIS PRO LEU ALA SER	PHE SER	PHE THR SER	ALA CYS	THR PHE	
	GGG ATC ATG AAC	TGT AGC	CAT CCC CTG GCC	TTC AGC	TTT ACC TCT GCA	TGT ACC	TTC	
290	ILE CYS SER GLU GLY	THR GLU LEU ILE GLY	LYS LYS	THR ILE CYS	GLU SER SER	GLY		
	ATC TGC TCA GAA GGA	ACT GAG TTA ATT GGG	AAG AAG	TGT GAA	TCA TCT GGA			
310	ILE TRP SER ASN PRO SER	PRO ILE CYS	GLN LYS LEU ASP	LYS SER PHE SER	MET ILE LYS			
	ATC TGG TCA AAT CCT AGT	CCA ATA TGT	CAA AAA TTG GAC	AAA AGT TTC TCA	ATG ATT AAG			
330	GLU GLY ASP TYR ASN PRO LEU PHE ILE PRO	VAL ALA VAL	MET VAL THR ALA PHE SER GLY					
	GAG GGT GAT TAT AAC CCC CTC TTC ATT CCA GTG GCA GTC	ATT CCA GTG GCA GTC	ATG GTT ACT GCA TTC TCT GGG					

FIG. 1B

340 STOP TRANSFER SEQUENCE

FIG. 1C

GAATTCTGGAGCTGGGACCCGGCCCTTCCTGGCAAGAACCTTGAGCCCCAGGTGGCAGGGAGGGCTGAGGCCCTGGCACAG

AGACTTGCAGAGACCCAGCAAGCC	1	MET	VAL	PHE	PRO	TRP	ARG	CYS	GLU	GLY	THR	TYR	TRP	GLY
		ATG	GTG	TTT	CCA	TGG	AGA	TGT	GAG	GGT	ACT	TAC	TGG	GGC

1	MET	VAL	PHE	PRO	TRP	ARG	CYS	GLU	GLY	THR
10	CC	ATG	GTG	TTT	CCA	TGG	AGA	TGT	GAG	GGT
20	SIGNAL SEQUENCE									
30										

FIG.2A

N-TERMINUS										40	50								
HIS	GLY	THR	HIS	CYS	TRP	THR	TYR	HIS	TYR	SER	GLU	LYS	PRO	MET	ASN	TRP	GLU	ASN	ALA
CAT	GGA	ACT	CAC	TGT	TGG	ACT	TAC	CAT	TAT	TCT	GAA	AAG	CCC	ATG	AAC	TGG	GAA	AAT	GCT

GLU TYR LEU GLU ASN THR LEU PRO LYS SER PRO TYR TYR TYR TRP ILE GLY ILE ARG LYS
GAG TAT TTA GAG AAT ACA TTG CCC AAA AGC CCT TAT TAC TAC TGG ATA GGA ATC AGG AAA

ILE	GLY	LYS	MET	TRP	THR	TRP	VAL	GLY	THR	ASN	LYS	THR	LEU	THR	LYS	GLU	ALA	GLU	ASN
ATT	GGG	AAA	ATG	TGG	ACA	TGG	GTG	GGA	ACC	AAC	AAA	ACT	CTC	ACT	AAA	GAA	GCA	GAG	AAC

LYS	ARG	GLU	ARG	ASP	SER	GLY	LYS	TRP	ASN	ASP	ASP	ALA	CYS	HIS	LYS	ARG	LYS	ALA	ALA
AAG	AGG	GAA	CGA	GAC	TCT	GGG	AAA	TGG	AAC	GAT	GAC	GCC	TGT	CAC	AAA	CGA	AAG	GCA	GCT

LEU **CYS** TYR THR ALA SER **CYS** GLN PRO GLY SER **CYS** ASN GLY ARG GLY GLU **CYS** VAL GLU
 CTC **TGC** TAC ACA GCC TCT **TGC** CAG CCA GGG TCT **TGC** AAT GCC CGT GGA GAA **TGT** GTG GAA 160
 170
 THR ILE ASN **ASN HIS THR** **CYS** ILE **CYS** ASP ALA GLY TYR TYR GLY PRO GLN **CYS** GLN TYR
 ACT ATC AAC **AAT CAC ACG** **TGC** ATC **TGT** GAT GCA GGG TAT TAC GGG CCC CAG **TGT** CAG TAT 180
 190
 VAL VAL GLN **CYS** GLU PRO LEU GLU ALA PRO GLU LEU GLY THR MET ASP **CYS** ILE HIS PRO
 GTG GTC CAG **TGT** GAG CCT TTG GAG GCC CCT GAG TTG GGT ACC ATG GAC **TGC** ATC CAC CCC 200
 210
 LEU GLY ASN PHE SER PHE GLN SER LYS **CYS** ALA PHE **ASN CYS SER** GLU GLY ARG GLU LEU
 TTG GGA AAC TTC AGC TTC CAG TCC AAG **TGT** GCT **TTC** AAC TGT TCT GAG GGA AGA GAG CTA 220
 230
 LEU GLY THR ALA GLU THR GLN **CYS** GLY ALA SER GLY **ASN TRP SER** SER PRO GLU PRO ILE
 CTT GGG ACT GCA GAA ACA CAG **TGT** GGA GCA TCT GGA **AAC TGG TCA** TCT CCA GAG CCA ATC 240
 250
 CYS GLN VAL VAL GLN **CYS** GLU PRO LEU GLU ALA PRO GLU LEU GLY THR MET ASP **CYS** ILE
 TGC CAA GTG GTC CAG **TGT** GAG CCT TTG GAG GCC CCT GAG TTG GGT ACC ATG GAC **TGC** ATC 260
 270
 HIS PRO LEU GLY ASN PHE SER PHE GLN SER LYS **CYS** ALA PHE **ASN CYS SER** GLU GLY ARG
 CAC CCC TTG GGA AAC TTC AGC TTC CAG TCC AAG **TGT** GCT **TTC** AAC TGT TCT GAG GGA AGA 280
 290
 GLU LEU LEU GLY THR ALA GLU THR GLN **CYS** GLY ALA SER GLY **ASN TRP SER** SER PRO GLU
 GAG CTA CTT GGG ACT GCA GAA ACA CAG **TGT** GGA GCA TCT GGA **AAC TGG TCA** TCT CCA GAG 300
 310
 PRO ILE **CYS** GLN GLU THR ASN ARG SER PHE SER LYS ILE LYS GLU GLY ASP TYR ASN **PRO**
 CCA ATC **TGC** CAA GAG ACA **AC AGA AGT** TTC TCA AAG ATC AAA GAA GGT GAC TAC AAC **CCC** 320
 330

FIG.2B

		STOP TRANSFER SEQUENCE																	
		340					350												
LEU	PHE	ILE	PRO	VAL	ALA	MET	VAL	THR	ALA	PHE	SER	GLY	LEU	ALA	PHE	LEU	ILE	TRP	
CTC	TTC	ATT	CCT	GTA	GCC	GTC	ATG	GTC	ACC	GCA	TTC	TCG	GGG	CTG	GCA	TTT	CTC	ATT	TGG
LEU	ALA	ARG	ARG	LEU	LYS	GLY	LYS	SER	GLN	GLU	ARG	MET	ASP	ASP	PRO	TYR	OP		
CTG	GCA	AGG	CGG	TTA	AAA	AAA	GGC	AAG	AAA	TCT	CAA	GAA	AGG	ATG	GAT	CCA	TAC	TGA	
TTT	CAT	CCT	TG	GA	AG	GA	AA	GC	CA	AG	TC	AA	GT	CA	AG	TG	CC	GT	GA
GCT	CCT	CCT	TA	AT	TT	CC	CT	CG	CT	AT	CC	AT	TA	AC	CC	CT	TT	CT	AC
TCAT	CTT	TCT	GTT	GG	AG	GA	CA	AA	AG	GT	T	TA	AG	AT	GG	AA	TT	CT	AC
TGTT	TCT	CA	TT	CAG	CAC	CAG	AA	AG	CT	TA	CT	GT	GT	CT	AT	CA	AG	GT	AT
ACT	CCT	GG	CAT	AG	TG	TA	CC	CT	AT	GT	AA	AC	AG	CT	GC	TT	TA	CT	CT
TCA	AG	TT	GG	AA	AG	TC	TA	CT	TC	GT	AG	CC	AC	TC	GT	AG	GT	TC	AC
TCCC	CAT	TCT	TT	CCT	TA	GG	GA	AT	AT	CC	AC	AC	AT	TC	GC	CC	AA	GA	GG
TCT	CCT	GC	ATT	G	TT	G	AT	TT	CC	CT	CT	TT	AT	TA	TT	CC	CT	TT	CT
GAT	GAT	T	TA	AT	G	A	T	A	C	A	C	A	C	A	C	AG	GT	AA	AT
CTGG	GG	CT	GG	GT	GA	CC	CT	TT	CC	CT	AA	CA	AT	CT	TC	TA	CT	AC	GA
GCT	GTC	CCC	CA	ACT	CT	TAC	CAT	GT	CTT	TAA	ACT	TC	CT	TC	TA	AA	TT	AG	AT
TTCA	CT	GC	AA	GG	TT	TA	AC	AT	GA	GA	TT	AA							

FIG.2C

		SIGNAL SEQUENCE																				
mHR		M V F P W R C E G T Y W G S R N I L K L W V W T L L C C D F L I H H G T H C W T Y H Y S E K P M N W																				
hHR		M I F P W K C Q S T Q R D L W N I F K L W G W T M L C C D F L A H H G T Y C W T Y H Y S E K P M N W																				
		LECTIN DOMAIN																				
mHR		E N A R K F C K Q N Y T D L V A I Q N K R E I E Y L E N T L P K S P Y Y W I G I R K I G K M W T W																				
hHR		Q R A R R F C R D N Y T D L V A I Q N K A E I E Y L E K T L P F S R S Y Y W I G I R K I G G I W T W																				
		EGF DOMAIN																				
mHR		V G T N K T L T K E A E N W G A G E P N N K K S K E D C V E I Y I K R E R D S G K W N D D A C H K R																				
hHR		V G T N K S L T E E A E N W G D G E P N N K K N K E D C V E I Y I K R N K D A G K W N D D A C H K L																				

FIG.3A

		COMPLEMENT BINDING REPEAT 1											
mHR	E A P E L G T M D C I H P L G N F S F Q S K C A F N C S E G R E L L G T A E T Q C G A S G N W S S P												
hHR	E A P E L G T M D C T H P F G N F S F S S O C A F S C S E G T N L T G I E E T T C G P F G N W S S P												
		COMPLEMENT BINDING REPEAT 2											
mHR	T Q C G A S G N W S S P E P I C Q E T N R S F S K I K E G D Y N P L F I P V A V M V T A F S G L A F												
hHR	T I C E S S G i W S S P E P I C Q K L D K S F S M I K E G D Y N P L F I P V A V M V T A F S G L A F												
		TRANSMEMBRANE DOMAIN											
mHR	L I W L A R R L K K G K K S Q E R M D D P Y												
hHR	I I W L A R R L K K G K K S K R S M N D P Y												

FIG.3B

CYTOPLASMIC DOMAIN

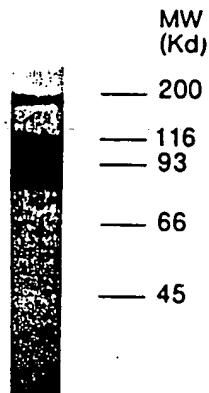


FIG.4A

1 T H K M K F K VVIL K
 10 20 30
 XTYHYSEKPMNWENARKFXKQNYTDLVAIQNKXXIEYL

FIG.4B

5' A A C A G A A T G C C C T G G G A G A A T G C 3'
 3' G A G A A G C C C A T G A A T T G G G A G A A T G C

FIG.4C

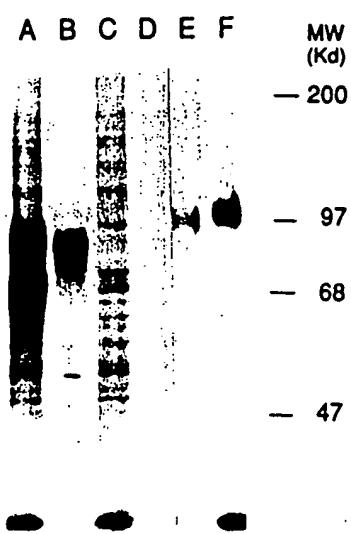


FIG. 5

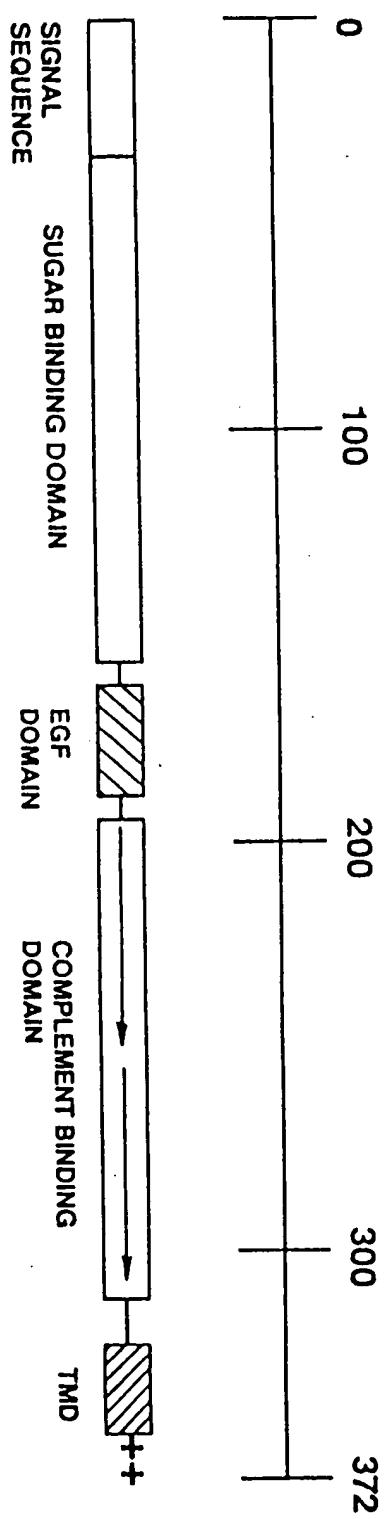


FIG. 6